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Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a

FEATURES Location/Qualifiers
 source 1. .20
 /organism="unknown"
 BASE COUNT 7 a 4 c 6 g 3 t

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORIGIN

Qy 1 CCTGAACTAGGAACCAAGATG 20
 Db 1 CCTGAACTAGGAACCAAGATG 20

RESULT 2
 A91898 LOCUS A91898 27 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 2 from Patent EP0849364.
 ACCESSION A91898 GI:6740771
 VERSION 1
 KEYWORDS unidentified
 SOURCE ORGANISM unidentified
 unclassified
 1 (bases 1 to 27)
 REFERENCE Paapebo, S.B. and Kilger, C.A.
 AUTHORS Kilger, C. and Motz, M.
 TITLE Method for the direct, exponential amplification and sequencing of
 DNA molecules and its application
 JOURNAL Patent: EP 0849364 A 2 24-JUN-1998;
 BOHRINGER MANNHEIM GMBH (DE)
 FEATURES Location/Qualifiers
 SOURCE 1. .27
 /organism="unidentified"
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 BASE COUNT 9 a 5 c 7 g 6 t

ORIGIN

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Qy 1 CCTGAACTAGGAACCAAGATG 20
 Db 1 CCTGAACTAGGAACCAAGATG 27

RESULT 5
 AX032401 LOCUS AX032401 27 bp DNA linear PAT 24-NOV-2000
 DEFINITION Sequence 2 from Patent EP1004677.
 ACCESSION AX032401 AX032401
 VERSION 1 (bases 1 to 27)
 KEYWORDS unidentified
 SOURCE ORGANISM unidentified
 unclassified
 1
 REFERENCE Paapebo, S.E. and Kilger, C.A.
 AUTHORS Kilger, C. and Motz, M.
 TITLE Method for the direct, exponential amplification and
 JOURNAL Patent: EP 1004677-A 2 31-MAY-2000;
 ROCHE DIAGNOSTICS GMBH (DE)
 FEATURES COMMENT
 On Oct 15, 2002 this sequence version replaced GI:10279380.
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ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 27;
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Qy 1 CCTGAACTAGGAACCAAGATG 20
 Db 1 CCTGAACTAGGAACCAAGATG 27

RESULT 6
 AX137492 LOCUS AX137492 27 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 2 from Patent EP1091002.
 ACCESSION AX137492

Query Match 100.0%; Score 20; DB 6; Length 27;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAACTAGGAACCAAGATG 27
 Db 1 CCTGAACTAGGAACCAAGATG 27